

(B)

Tue Jul 17 13:23:35 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpanda/temp1/p1.DNA32292.nc (353 aa)

Sequences producing High-scoring Segment Pairs:			Score	Match	Pct	E-val
1	P_AAB53075	Human angiogenesis-associated protein PRO	2005	353	100	0.0
2	P_AAB61231	Human TANGO 331 protein - Homo sapiens.	2005	353	100	0.0
3	P_AAB80212	Human PRO211 protein - Homo sapiens.	2005	353	100	0.0
4	P_AAB68596	PRO211 - Homo sapiens.	2005	353	100	0.0
5	P_AAY83224	PRO211 Polypeptide - Homo sapiens.	2005	353	100	0.0
6	P_AAB00169	PRO211 polypeptide - Homo sapiens.	2005	353	100	0.0
7	P_AAY05283	EGF-like homologue PRO211 - Homo sapiens.	2005	353	100	0.0
8	P_AAY13344	protein PRO211 - Homo sapiens.	2005	353	100	0.0
9	P_AAY08064	Human EGF-like homologue protein (PRO217)	2005	353	100	0.0
10	P_AAY88571	Human PRO211 amino acid sequence - Homo s	1997	352	100	0.0
11	P_AAB61233	Mature human TANGO 331 protein - Homo sap	1887	329	100	0.0
12	AAH02894.114	Unknown (protein for MGC:11256) - Homo sa	1770	321	91	0.0
13	NP_077300.1	hypothetical protein MGC11256 - Homo sapi	1770	321	91	0.0
14	P_AAB42711	Human ORFX ORF2475 polypeptide sequence S	1716	298	97	0.0
15	P_AAY91870	Human apoptosis related protein - Homo sa	1635	301	85	0.0

BLAST RESULTS B-1

>1 P_AAB53075 Human angiogenesis-associated protein PRO211, SEQ ID NO:57 - Homo sapiens. (353 aa) [1 seg]

Score = 2005 (776 bits), Expect = 0.0

Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```
DNA32292.nc      1  MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAB53075      1  MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

DNA32292.nc     61  EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAB53075     61  EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

DNA32292.nc    121  VKTLK VCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
*****
P_AAB53075    121  VKTLK VCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC

DNA32292.nc    181  MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPP
*****
P_AAB53075    181  MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPP

DNA32292.nc    241  CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
*****
P_AAB53075    241  CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT

DNA32292.nc    301  CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB53075    301  CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
```

>2 P_AAB61231 Human TANGO 331 protein - Homo sapiens. (353 aa) [1 seg]

Score = 2005 (776 bits), Expect = 0.0

Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```
DNA32292.nc      1  MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
```

P_AAB61231 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

P_AAB61231 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

P_AAB61231 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

DNA32292.nc 181 MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PP

P_AAB61231 181 MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PP

DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT

P_AAB61231 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT

DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

P_AAB61231 301 CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

>3 P_AAB80212 Human PRO211 protein - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAB80212 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

P_AAB80212 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

P_AAB80212 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

DNA32292.nc 181 MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PP

P_AAB80212 181 MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PP

DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT

P_AAB80212 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT

DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

P_AAB80212 301 CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

>4 P_AAB68596 PRO211 - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAB68596 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

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BLAST RESULTS B-3

```
DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAB68596 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAB68596 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAB68596 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP

DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAB68596 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA

DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB68596 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
```

>5 P_AAY83224 PRO211 Polypeptide - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```
DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY83224 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAY83224 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY83224 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY83224 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP

DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY83224 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA

DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY83224 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
```

>6 P_AAB00169 PRO211 polypeptide - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```
DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAB00169 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
```

```

DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPDLFEWFC
*****
P_AAB00169 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAB00169 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAB00169 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAB00169 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB00169 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****

```

>7 P_AAY05283 EGF-like homologue PRO211 - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY05283 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPDLFEWFC
*****
P_AAY05283 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY05283 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY05283 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY05283 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY05283 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****

```

>8 P_AAY13344 protein PRO211 - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY13344 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPDLFEWFC
*****

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BLAST RESULTS B-A

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*****
P_AAY13344 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY13344 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY13344 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY13344 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY13344 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

```

>9 P_AAY08064 Human EGF-like homologue protein (PRO217) encoded by DNA32292 cDNA
 - Homo sapiens. (353 aa) [1 seg]
 Score = 2005 (776 bits), Expect = 0.0
 Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY08064 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAY08064 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY08064 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY08064 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY08064 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY08064 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

```

>10 P_AAY88571 Human PRO211 amino acid sequence - Homo sapiens. (353 aa) [1 seg]
 Score = 1997 (773 bits), Expect = 0.0
 Identities = 352/353 (99%), Positives = 352/353 (99%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY88571 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

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BLAST RESULTS B-5

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*****
P_AAY88571    61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc   121 VKTLK VCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY88571    121 VKTLK VCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc   181 MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PP
*****
P_AAY88571    181 MDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PP
DNA32292.nc   241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
*****
P_AAY88571    241 CSAAQFCKMANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
DNA32292.nc   301 CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY88571    301 CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

```

>11 P_AAB61233 Mature human TANGO 331 protein - Homo sapiens. (329 aa) [1 seg]
Score = 1887 (731 bits), Expect = 0.0
Identities = 329/329 (100%), Positives = 329/329 (100%), at 25,1-353,329

```

DNA32292.nc   25 AKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWE EKTL SKYESSEIRLLEILEGLCE
*****
P_AAB61233    1 AKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWE EKTL SKYESSEIRLLEILEGLCE
DNA32292.nc   85 SSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LK VCCSPGTYGPDCLACQGG S
*****
P_AAB61233    61 SSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LK VCCSPGTYGPDCLACQGG S
DNA32292.nc   145 QRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHS ICTACDESK
*****
P_AAB61233    121 QRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHS ICTACDESK
DNA32292.nc   205 TCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PPSAAQFCKNANGSYTCEECDSSCV
*****
P_AAB61233    181 TCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP PPSAAQFCKNANGSYTCEECDSSCV
DNA32292.nc   265 GCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSYVCVCPDGF E
*****
P_AAB61233    241 GCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSYVCVCPDGF E
DNA32292.nc   325 ETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB61233    301 ETEDACVPPAEAEATEGESPTQLPSREDL

```

>12 AAH02894.114 Unknown (protein for MGC:11256) - Homo sapiens (321 aa) [1 seg]
Score = 1770 (686 bits), Expect = 0.0
Identities = 321/353 (90%), Positives = 321/353 (90%), Gaps = 32/353 (9%), at 1,1-353,321

```

DNA32292.nc   1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
AAH02894.114  1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc   61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

```

BLAST RESULTS B-U

```
*****
AAH02894.114 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
AAH02894.114 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
AAH02894.114 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
AAH02894.114 241 CSAAQFCKNANGSYTCE-----DVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
AAH02894.114 269 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
```

>13 NP_077300.1 hypothetical protein MGC11256 - Homo sapiens (321 aa) [1 seg]
Score = 1770 (686 bits), Expect = 0.0
Identities = 321/353 (90%), Positives = 321/353 (90%), Gaps = 32/353 (9%), at 1,1-353,321

```
DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
NP_077300.1 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
NP_077300.1 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
NP_077300.1 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
NP_077300.1 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
NP_077300.1 241 CSAAQFCKNANGSYTCE-----DVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
NP_077300.1 269 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
```

>14 P_AAB42711 Human ORFX ORF2475 polypeptide sequence SEQ ID NO:4950 - Homo
(318 aa) [1 seg]
Score = 1716 (665 bits), Expect = 0.0
Identities = 298/306 (97%), Positives = 298/306 (97%), at 20,2-325,307

```
DNA32292.nc 20 PAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLKSKYESSEIRLLEIL
**
P_AAB42711 2 PACPPGYLTAPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLKSKYESSEIRLLEIL
```

DNA32292.nc	80	EGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLA

P_AAB42711	62	EGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLA
DNA32292.nc	140	CQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTAC

P_AAB42711	122	CQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTAC
DNA32292.nc	200	DESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANGSYTCEEC

P_AAB42711	182	DESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANGSYTCEEC
DNA32292.nc	260	DSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSYVCVC

P_AAB42711	242	DSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSYVCVC
DNA32292.nc	320	PDGFEE

P_AAB42711	302	PDGFEE

>15 P_AAY91870 Human apoptosis related protein - Homo sapiens. (353 aa) [1 seg]
Score = 1635 (634 bits), Expect = 0.0
Identities = 301/354 (85%), Positives = 306/354 (86%), Gaps = 2/354 (0%), at
1,1-353,353

DNA32292.nc	1	MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAY91870	1	MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc	61	EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

P_AAY91870	61	EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc	121	VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC

P_AAY91870	121	VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
DNA32292.nc	181	MDGYFSSL-RNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP

P_AAY91870	181	MDGYFSSAPXTRPTASAPVTSPARRARGLDQQRRLA-ASVKWAGCWTRAPVWMWTSVRPT
DNA32292.nc	240	PCSAAQFCKNANGSYTCEECSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEK
		* *****
P_AAY91870	240	VPAACQFCKNPNGSYTCEECSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEK
DNA32292.nc	300	TCVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

P_AAY91870	300	TCVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

BLAST RESULTS B-8

(A)

Tue Jul 17 13:47:10 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpenda/templ/ss.DNA32292 (1364 bp)

Sequences producing High-scoring Segment Pairs:	Frame	Score	Match	Pct	E-val
1 P_AAC97409 Human angiogenesis-associated protein PR	+	1364	1364	100	0.0
2 P_AAF72371 Human PRO211 cDNA.	+	1364	1364	100	0.0
3 P_AAF60360 PRO211 coding sequence.	+	1364	1364	100	0.0
4 P_AAZ93700 PRO211 DNA32292-1131.	+	1364	1364	100	0.0
5 P_AAA30040 Human PRO211 nucleotide sequence.	+	1364	1364	100	0.0
6 P_AAA54089 PRO211 cDNA.	+	1364	1364	100	0.0
7 P_AAX28433 EGF-like homologue PRO211 coding sequenc	+	1364	1364	100	0.0
8 P_AAX52213 Protein PRO211 cDNA clone DNA32292-1131.	+	1364	1364	100	0.0
9 P_AAX37671 Human EGF-like homologue (PRO217) encode	+	1364	1364	100	0.0
10 AX076909 Sequence 21 from Patent WO0105836.	+	1364	1364	100	0.0
11 P_AAF29457 Human TANGO 331 cDNA.	+	1350	1350	100	0.0
12 P_AAA08503 DNA encoding human apoptosis related pro	+	1290	1358	99	0.0
13 P_AAC76920 Human OREF ORF2475 polynucleotide sequen	+	1208	1215	100	0.0

>1 P_AAC97409 Human angiogenesis-associated protein PRO211 cDNA, SEQ ID NO:56.
(1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292	1	GGCCGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
P_AAC97409	1	GGCCGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
P_AAC97409	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
P_AAC97409	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
P_AAC97409	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
P_AAC97409	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
P_AAC97409	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
P_AAC97409	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
P_AAC97409	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

BLAST REPORT RESULTS A-1

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*****
P_AAC97409 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292 541 CAGACAGGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
*****
P_AAC97409 541 CAGACAGGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAC97409 601 CTGCATGGACGGCTACTTCAGCTCGTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAC97409 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
P_AAC97409 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAC97409 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
*****
P_AAC97409 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
*****
P_AAC97409 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAC97409 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAC97409 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAC97409 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCAAGACCTGTAATGTGCCGGACTTAC
DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAC97409 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
*****
P_AAC97409 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAC97409 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****

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BLAST RESULTS A-2

P_AAC97409 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>2 P_AAF72371 Human PRO211 cDNA. (1825 bp) [1 seg]
 Score = 1364 (2704 bits), Expect = 0.0
 Identities = 1364/1364 (100%), at 1,75-1364,1438, Strand +/+

DNA32292	1	GGCCGGAGCAGCACGGCCGAGGACCTGGAGTCCGGCTGCGTCTTCCCGCAGCGCTACC

P_AAF72371	75	GGCCGGAGCAGCACGGCCGAGGACCTGGAGTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAF72371	135	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAF72371	195	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

P_AAF72371	255	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT

P_AAF72371	315	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAF72371	375	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

P_AAF72371	435	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGAACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

P_AAF72371	495	TTGTGTGAAGAACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

P_AAF72371	555	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA

P_AAF72371	615	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

P_AAF72371	675	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

P_AAF72371	735	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAF72371	795	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

BLAST RESULTS #3

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DNA32292      781 TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAF72371    855 TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

DNA32292      841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC
*****
P_AAF72371    915 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC

DNA32292      901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
*****
P_AAF72371    975 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA

DNA32292      961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAF72371    1035 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292      1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAF72371    1095 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292      1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAF72371    1155 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCAAGACCTGTAATGTGCCGGACTTAC

DNA32292      1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAF72371    1215 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292      1201 GCAGTGGACAGCGGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC
*****
P_AAF72371    1275 GCAGTGGACAGCGGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC

DNA32292      1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTT
*****
P_AAF72371    1335 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTT

DNA32292      1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAF72371    1395 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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BLAST RESULTS A-4

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>3 P_AAF60360 PRO211 coding sequence. (1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

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DNA32292      1  GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAF60360     1  GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292      61  CGCCATGCGCCTGCCGCGCCGGGCCGCGTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAF60360     61  CGCCATGCGCCTGCCGCGCCGGGCCGCGTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292      121  GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAF60360     121  GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

```

DNA32292	181	CAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
P_AAF60360	181	CAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
P_AAF60360	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
P_AAF60360	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
P_AAF60360	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
P_AAF60360	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
P_AAF60360	481	ATGCCAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
P_AAF60360	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
P_AAF60360	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
P_AAF60360	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
P_AAF60360	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
P_AAF60360	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
P_AAF60360	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
P_AAF60360	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
P_AAF60360	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

BLAST RESULTS A-5

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*****
P_AAF60360 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292 1081 AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAF60360 1081 AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAF60360 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
*****
P_AAF60360 1201 GCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAF60360 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAF60360 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

```

>4 P_AAZ93700 PRO211 DNA32292-1131. (1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

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DNA32292 1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAZ93700 1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAZ93700 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAZ93700 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAZ93700 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
*****
P_AAZ93700 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAZ93700 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAZ93700 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****

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BLAST RESULTS A-6

P_AA93700	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
P_AA93700	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCTGCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
P_AA93700	541	CAGACAGGGCGACGGGTCTGCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
P_AA93700	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
P_AA93700	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
P_AA93700	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
P_AA93700	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
P_AA93700	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
P_AA93700	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
P_AA93700	961	AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
P_AA93700	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
P_AA93700	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
P_AA93700	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
P_AA93700	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292	1261	TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
P_AA93700	1261	TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

BLAST RESULTS A-7

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DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAAA
*****
P_AA293700 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAAA

>5 P_AAA30040 Human PRO211 nucleotide sequence. (1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292 1 GGCCGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAA30040 1 GGCCGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAA30040 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCGCGCGCCGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAA30040 121 GCGCGCGCCGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAA30040 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
*****
P_AAA30040 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAA30040 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAA30040 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAA30040 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

DNA32292 481 ATGCCAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAA30040 481 ATGCCAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

DNA32292 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
*****
P_AAA30040 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA

DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAA30040 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAA30040 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

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BLAST RESULTS A-B

DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAA30040	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

P_AAA30040	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC

P_AAA30040	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA

P_AAA30040	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

P_AAA30040	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

P_AAA30040	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

P_AAA30040	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT

P_AAA30040	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

P_AAA30040	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292	1261	TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

P_AAA30040	1261	TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292	1321	TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

P_AAA30040	1321	TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>6 P_AAA54089 PRO211 cDNA. (1364 bp) [1 seg]

Score = 1364 (2704 bits), Expect = 0.0

Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292	1	GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

P_AAA54089	1	GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
		*-*****
P_AAA54089	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

BLAST RESULTS A-9

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*****
P_AAA54089 121 GCCCGCGCCGGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAAGCTTTGGCGGCGGGAACACGGC
*****
P_AAA54089 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAAGCTTTGGCGGCGGGAACACGGC
DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCT
*****
P_AAA54089 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCT
DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAA54089 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAA54089 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAA54089 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAA54089 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
*****
P_AAA54089 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAA54089 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAA54089 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
P_AAA54089 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAA54089 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292 841 TGACTIONAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
*****
P_AAA54089 841 TGACTIONAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
*****
P_AAA54089 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292 961 AACCTGTGTGAGGAAAAACGAAAAGTCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****

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BLAST RESULTS A-10

P_AAA54089 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

P_AAA54089 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

P_AAA54089 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT

P_AAA54089 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

P_AAA54089 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

DNA32292 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

P_AAA54089 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

P_AAA54089 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>7 P_AAX28433 EGF-like homologue PRO211 coding sequence. DNA, PAT 22-JUN-1999
(1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

P_AAX28433 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAX28433 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAX28433 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAAGCTTTGGCGGCGGGAACACGGC

P_AAX28433 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAAGCTTTGGCGGCGGGAACACGGC

DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

P_AAX28433 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAX28433 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

BLAST RESULTS A11

P_AAX28433	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC *****
P_AAX28433	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG *****
P_AAX28433	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA *****
P_AAX28433	541	CAGACAGGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG *****
P_AAX28433	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT *****
P_AAX28433	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC *****
P_AAX28433	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG *****
P_AAX28433	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC *****
P_AAX28433	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA *****
P_AAX28433	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG *****
P_AAX28433	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC *****
P_AAX28433	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC *****
P_AAX28433	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT *****
P_AAX28433	1141	CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC *****
P_AAX28433	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC

BLAST RESULTS A-12

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DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAX28433 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAX28433 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>8 P_AAX52213 Protein PRO211 cDNA clone DNA32292-1131. DNA, PAT 25-JUN-1999
(1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/+

DNA32292 1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAX52213 1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAX52213 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAX52213 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAX52213 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
*****
P_AAX52213 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAX52213 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAX52213 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAX52213 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

DNA32292 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAX52213 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

DNA32292 541 CAGACAGGGCGACGGGTCCGCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
*****
P_AAX52213 541 CAGACAGGGCGACGGGTCCGCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA

DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAX52213 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

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BLAST RESULTS A-13

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DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAX52213 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
P_AAX52213 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAX52213 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTC
*****
P_AAX52213 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTC

DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
*****
P_AAX52213 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA

DNA32292 961 AACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAX52213 961 AACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAX52213 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAX52213 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAX52213 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
*****
P_AAX52213 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

DNA32292 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAX52213 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAX52213 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

```

>9 P_AAX37671 Human EGF-like homologue (PRO217) encoded by DNA32292 cDNA. (1364 bp) [1 seg]

Score = 1364 (2704 bits), Expect = 0.0

Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/+

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DNA32292 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAX37671 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

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DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAX37671	61	CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAX37671	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

P_AAX37671	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

P_AAX37671	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAX37671	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTT

P_AAX37671	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

P_AAX37671	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

P_AAX37671	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA

P_AAX37671	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

P_AAX37671	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

P_AAX37671	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAX37671	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

P_AAX37671	781	TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

P_AAX37671	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

BLAST RESULTS A-15

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DNA32292  901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
*****
P_AAX37671 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA

DNA32292  961 AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAX37671 961 AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292  1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAX37671 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292  1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAX37671 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

DNA32292  1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAX37671 1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292  1201 GCAGTGGACACGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC
*****
P_AAX37671 1201 GCAGTGGACACGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC

DNA32292  1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAX37671 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292  1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAX37671 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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>10 AX076909 Sequence 21 from Patent WO0105836. (1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

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DNA32292  1  GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
AX076909  1  GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292  61  CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
AX076909  61  CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292  121  GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
AX076909  121  GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292  181  CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
AX076909  181  CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

DNA32292  241  TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
*****
AX076909  241  TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292  301  GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

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BLAST RESULTS A-110

AX076909	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
AX076909	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
AX076909	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
AX076909	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
AX076909	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
AX076909	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
AX076909	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
AX076909	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
AX076909	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
AX076909	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
AX076909	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
AX076909	961	AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
AX076909	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
AX076909	1081	AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT

BLAST RESULTS A-17

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AX076909 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC
*****
AX076909 1201 GCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTT
*****
AX076909 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTT
DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
AX076909 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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>11 P_AAF29457 Human TANGO 331 cDNA. (1432 bp) [1 seg]
Score = 1350 (2676 bits), Expect = 0.0
Identities = 1350/1350 (100%), at 1,50-1350,1399, Strand +/-

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DNA32292      1  GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAF29457    50  GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292     61  CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAF29457   110  CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292    121  GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAF29457   170  GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292    181  CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAF29457   230  CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292    241  TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
*****
P_AAF29457   290  TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
DNA32292    301  GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAF29457   350  GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292    361  GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAF29457   410  GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292    421  TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAF29457   470  TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292    481  ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAF29457   530  ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292    541  CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
*****
P_AAF29457   590  CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA

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BLAST RESULTS A-B

DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

P_AAF29457	650	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

P_AAF29457	710	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAF29457	770	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

P_AAF29457	830	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

P_AAF29457	890	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA

P_AAF29457	950	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

P_AAF29457	1010	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

P_AAF29457	1070	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

P_AAF29457	1130	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

P_AAF29457	1190	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

P_AAF29457	1250	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292	1261	TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

P_AAF29457	1310	TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292	1321	TGTAATAAAATTGACCATTGTAGGTAATCA

P_AAF29457	1370	TGTAATAAAATTGACCATTGTAGGTAATCA

BLAST RESULTS A-19

>12 P_AAA08503 DNA encoding human apoptosis related protein. (1380 bp) [1 seg]
 Score = 1290 (2557 bits), Expect = 0.0
 Identities = 1358/1369 (99%), Gaps = 10/1369 (0%), at 1,10-1364,1373, Strand
 +/-

DNA32292	1	GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
P_AAA08503	10	GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
P_AAA08503	70	CGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
P_AAA08503	130	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
P_AAA08503	190	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGCTGGAGATCCT
P_AAA08503	250	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
P_AAA08503	310	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
P_AAA08503	370	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
P_AAA08503	430	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
P_AAA08503	490	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
P_AAA08503	550	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCT-CGCTCCGG-AACGAGACCCACAGCATCTGCACAGCC
P_AAA08503	610	CTGCATGGACGGCTACTTCAGCTCCGCTCCGGRAACGAGACCCACAGCATCTGCACAGCC
DNA32292	659	TGTGACGAGTCCTGCAAGACGTGCTC-GGGCCT-GACCAACAGAGAC-TGCGGCGAGTGT
P_AAA08503	670	TGTGACGAGTCCTGCAAGACGTGCTCGGGGCTGGACCAACAGAGACTTGCGGCGAGTGT
DNA32292	716	GAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAG
P_AAA08503	730	GAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGA-
DNA32292	776	CCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAA
P_AAA08503	789	CCG--TCCCTGCAGCG-TGC-CAGTTCTGTAAGAACCCCAACGGCTCCTACACGTGCGAA

BLAST RESULTS A-20

DNA32292	836	GAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGT
P_AAA08503	845	GAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGT
DNA32292	896	ATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCA
P_AAA08503	905	ATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCA
DNA32292	956	GAAAAAACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTACGTCTGT
P_AAA08503	965	GAAAAAACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTACGTCTGT
DNA32292	1016	GTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAA
P_AAA08503	1025	GTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAA
DNA32292	1076	GCCACAGAAGGAGAAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGA
P_AAA08503	1085	GCCACAGAAGGAGAAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGA
DNA32292	1136	CTTACCCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGT
P_AAA08503	1145	CTTACCCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGT
DNA32292	1196	CTCCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTT
P_AAA08503	1205	CTCCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTT
DNA32292	1256	GTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAG
P_AAA08503	1265	GTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAG
DNA32292	1316	TTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
P_AAA08503	1325	TTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>13 P_AAC76920 Human ORFX ORF2475 polynucleotide sequence SEQ ID NO:4949. (1259 bp) [1 seg]

Score = 1208 (2395 bits), Expect = 0.0

Identities = 1215/1216 (99%), Gaps = 1/1216 (0%), at 150,32-1364,1247, Strand +/+

DNA32292	150	CGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAACCAGGGGATGGTGGACACCG
P_AAC76920	32	CGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAACCAGGGGATGGTGGACACCG
DNA32292	210	CAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAAGACGCTGTCCAAGTACG
P_AAC76920	92	CAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAAGACGCTGTCCAAGTACG
DNA32292	270	AGTCCAGCGAGATTTCGCTGCTGGAGATCCTGGAGGGGCTGTGCGAGAGCAGCGACTTCG
P_AAC76920	152	AGTCCAGCGAGATTTCGCTGCTGGAGATCCTGGAGGGGCTGTGCGAGAGCAGCGACTTCG
DNA32292	330	AATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTGGCTGCAGCTGA
P_AAC76920	212	AATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTGGCTGCAGCTGA

BLAST RESULTS A-21

DNA32292	390	AGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGTGTGCTGCT
P_AAC76920	272	AGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGTGTGCTGCT
DNA32292	450	CTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGCA
P_AAC76920	332	CTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGCA
DNA32292	510	GCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTGCC
P_AAC76920	392	GCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTGCC
DNA32292	570	ACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCC
P_AAC76920	452	ACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCC
DNA32292	630	GGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCC
P_AAC76920	512	GGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCC
DNA32292	690	TGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTG
P_AAC76920	572	TGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTG
DNA32292	750	TGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGA
P_AAC76920	632	TGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGA
DNA32292	810	ACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGG
P_AAC76920	692	ACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGG
DNA32292	870	AAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTG
P_AAC76920	752	AAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTG
DNA32292	930	CAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACGAAAACCTGCT
P_AAC76920	812	CAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACGAAAACCTGCT
DNA32292	990	ACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTCTGACGGCTTCGAAGAA-ACGGAAGAT
P_AAC76920	872	ACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTCTGACGGCTTCGAAGAANACGGAAGAT
DNA32292	1049	GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCC
P_AAC76920	932	GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCC
DNA32292	1109	TCCCGCGAAGACCTGTAATGTGCCGACTTACCCTTTAAATTATTCAGAAGGATGTCCCG
P_AAC76920	992	TCCCGCGAAGACCTGTAATGTGCCGACTTACCCTTTAAATTATTCAGAAGGATGTCCCG
DNA32292	1169	TGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
P_AAC76920	1052	TGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC

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DNA32292	1229	CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCT

P_AAC76920	1112	CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCT
DNA32292	1289	TAAACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAAT

P_AAC76920	1172	TAAACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAAT
DNA32292	1349	CAGGAGGAAAAAAAAA

P_AAC76920	1232	CAGGAGGAAAAAAAAA

BLAST RESULTS A-23